

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/569,959
Source: IFWO
Date Processed by STIC: 11/30/2006

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 11/30/2006

PATENT APPLICATION: US/10/569,959

TIME: 13:29:16

Input Set : N:\efs\11_30_06\10569959_efs\pto.da.txt

Output Set: N:\CRF4\11302006\J569959.raw

3 <110> APPLICANT: Kabushiki Kaisha Hayashibara Seibutsu Kagaku Kenkyujo
 5 <120> TITLE OF INVENTION: Cyclic maltosylmaltose, cyclic maltosylmaltose-forming
 enzyme, their
 6 preparation and uses
 8 <130> FILE REFERENCE: 10102802
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/569,959
 C--> 10 <141> CURRENT FILING DATE: 2006-02-28
 10 <160> NUMBER OF SEQ ID NOS: 10
 12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 5
 14 <212> TYPE: PRT
 15 <213> ORGANISM: Arthrobacter globiformis
 17 <400> SEQUENCE: 1
 18 Asp Pro Thr Thr Ser
 19 1 5
 21 <210> SEQ ID NO: 2
 22 <211> LENGTH: 583
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Arthrobacter globiformis
 26 <400> SEQUENCE: 2
 27 Asp Pro Thr Thr Ser Pro Gly Pro Leu Ala Glu Gly Asp Val Ile Tyr
 28 1 5 10 15
 29 Gln Val Leu Val Asp Arg Phe Glu Asp Gly Asp Pro Thr Asn Asn Asp
 30 20 25 30
 31 Gln Gly Asp Gly Glu Tyr Asp Pro Ser Asp Leu Gly Phe Tyr His Gly
 32 35 40 45
 33 Gly Asp Trp Ala Gly Leu Thr Asp Arg Leu Asp Tyr Ile Ala Asp Leu
 34 50 55 60
 35 Gly Val Thr Ala Ile Trp Leu Ser Pro Val Ser Glu Gln Gln Pro Leu
 36 65 70 75 80
 37 Ser Arg Asp Gly Leu Glu Ala Ser Tyr His Gly Tyr Phe Thr Arg Asp
 38 85 90 95
 39 Phe Ala Thr Pro Asn Glu His Phe Gly Asp Arg Ala Glu Leu Gln Glu
 40 100 105 110
 41 Leu Ile Asp Thr Ala His Asp Leu Gly Leu Lys Met Ile Leu Asp Val
 42 115 120 125
 43 Val Pro Asn His Thr Ala Asp Tyr Leu Ala Gly Thr Ser Thr Thr Tyr
 44 130 135 140
 45 Ser Pro Ser Thr Tyr Lys Pro Ala Ser Pro Leu Asp Asp Ala Ser Tyr
 46 145 150 155 160
 47 Phe His His Ala Gly Asp Cys Leu Phe Asn Gly Leu Glu Thr Gln Thr
 48 165 170 175
 49 Gln Ile Glu Asn Cys Asp Leu Gly Gly Leu Asp Asp Leu Asp Gln Ser
 50 180 185 190

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51 Asn Pro Val Val Ser Ser His Leu Met Ser Thr Tyr Lys Asp Trp Val
52      195      200      205
53 Asp Met Gly Phe Asp Gly Ile Arg Val Asp Ala Ala Arg Ser Val Pro
54      210      215      220
55 Lys Pro Trp Leu Ala Asp Phe Glu Ala Glu Met Gly Val Pro Thr Phe
56 225      230      235      240
57 Gly Glu Val Phe Val Gly Asp Val Asp Tyr Val Ser Glu Tyr Gln Asp
58      245      250      255
59 Tyr Glu Trp Gly Val Leu Asp Phe Pro Tyr Phe Phe Thr Val Arg Glu
60      260      265      270
61 Ala Phe Ser Ala Asp Thr Asp Met Asn Lys Leu Gly Asp Leu Phe Asp
62      275      280      285
63 Gln Asp Ser Lys Tyr Ala Asn Pro Asn Arg Leu Glu Thr Phe Leu Asp
64      290      295      300
65 Asn His Asp Arg Ala Arg Phe Leu Thr Trp Ala Asp Asp Asn Tyr Gln
66 305      310      315      320
67 Arg Leu Arg Ser Gly Leu Thr Phe Leu Leu Thr Ser Arg Gly Val Pro
68      325      330      335
69 Val Ile Tyr Tyr Gly Thr Glu Gln Ala Asp Asp Gly Asn Gly Asn Pro
70      340      345      350
71 Tyr Glu Val Pro Ile Ala Asn Lys Asp Asn Arg Lys Asp Met Glu Ser
72      355      360      365
73 Phe Asp Gln Asn Ser Asn Leu Tyr Lys His Ile Gln Arg Leu Thr Ala
74      370      375      380
75 Ile Lys Ala Ala Tyr Pro Ala Leu Gln Val Gly Thr Gln Arg Glu Met
76 385      390      395      400
77 Trp Ser Asp Thr Ser Val Tyr Gly Phe Ser Arg Arg Val Asp Ser Thr
78      405      410      415
79 Gly Ala Glu Ala Met Thr Phe Ser Ser Asn Ser Trp Thr Thr Gln Thr
80      420      425      430
81 Arg Thr Val Pro Leu Arg Ala Glu Ser Ser Ile Thr Val Gly Thr Thr
82      435      440      445
83 Leu Thr Asn Leu Met Asn Thr Gly Asp Thr Val Thr Val Thr Ala Gly
84      450      455      460
85 Gly Val Thr Gly Lys Gln Ile Thr Val Ser Leu Gly Glu His Glu Ser
86 465      470      475      480
87 Lys Val Tyr Ala Pro Gly Thr Pro Val Ser Ala Tyr Ser Pro Glu Ala
88      485      490      495
89 Arg Asn Thr Thr Lys Ile Arg Val His Tyr Asn Val Gly Leu Gly His
90      500      505      510
91 Ser Ile Ala Ile Arg Gly Asp Glu Tyr Pro Phe Thr Trp Thr Ser Gly
92      515      520      525
93 Arg Gly Ala Arg Asn Val Ala Ser Asp Val Trp Glu Phe Glu Val Glu
94      530      535      540
95 Arg Ile Pro Asp Gly Glu Thr Phe Gln Phe Lys Pro Leu Ile Asp Asp
96 545      550      555      560
97 Val Thr Trp Ser Thr Gly Gly Asn Phe Thr Gly Thr Gly Gly Asp Val
98      565      570      575
99 Ile Asp Ile Tyr Pro Thr Phe

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100          580          583
102 <210> SEQ ID NO: 3
103 <211> LENGTH: 1749
104 <212> TYPE: DNA
105 <213> ORGANISM: Arthrobacter globiformis
107 <400> SEQUENCE: 3
108 gacccaccca cgctgcccgg cccgctggcc gagggcgacg tgatctacca ggtgctcgtc      60
109 gaccgggttcg aagacggcga cccacccaac aacgaccagg gcgacggaga gtacgatccg      120
110 tccgacctcg gtttctacca cggcggcgac tgggcgggcc tgacggaccg gctcgactac      180
111 atcgccgatc tgggtgtgac ggcgatctgg ctctcgcccg tctccgagca gcagccgctc      240
112 tcgcgcgacg ggctggaggc cagctaccac ggctacttca ctcgggactt cgcgacgccg      300
113 aacgagcatt tcggcgaccg agccgagctg caggagctga tcgacacggc gcacgatctc      360
114 ggactcaaga tgatcctcga cgctgtgccg aaccacacgg ccgactacct cgcgggcaca      420
115 tcgacgacct attcgccgag cacctacaag ccggcgagtc cgctcgatga cgcgtcgtac      480
116 ttccatcacg ccggcgactg cctgttcaac gggctcgaga cgcagacca gatcgagaac      540
117 tgcgacctcg gcgggctcga cgacctcgat cagtcgaacc cggctcgtctc gtcgcacctg      600
118 atgagcacgt acaaggactg ggtcgacatg ggcttcgacg gcatccgggt cgatgcggcg      660
119 cgctcggtgc cgaagccgtg gctcgccgac ttcgaagccg agatgggctg gccgaccttc      720
120 ggcgaggtgt tcgtcggcga tgcgaactac gtctcgaggt accaggacta cgagtggggc      780
121 gtgctcgact tccctactt cttcacggtg cgcgagggct tctcggccga taccgacatg      840
122 aacaagctcg gcgacctctt cgaccaggac agcaagtacg cgaacccgaa ccggctggag      900
123 acgttcctcg acaaccacga tcgggcgcgg ttctctacct gggccgatga caactatcag      960
124 cggctgcgct caggactgac gttcctccta acctcccggg gcgtgcccgt gatctactac      1020
125 ggcaccgagc aggcgcagca cggcaacggc aacccttacg aggtaccgat cgcgaacaag      1080
126 gacaaccgca aggacatgga gagcttcgat cagaactcga acctctacaa gcacatccag      1140
127 cggttgaccg cgatcaaggc cgcttaccgg gctctgcagg tcggcacaca gcgcgagatg      1200
128 tggtcgcgca cctccgtcta cgggttctcg cgacgcgtcg acagcacggg tgccgaggcg      1260
129 atgaccttct cgtcgaactc gtggacgacg cagacgcgca cggtgccgct gcgcgccgag      1320
130 agctcgatca cggtcggtac gacgctgacg aacctcatga acacgggcga cacggtgacc      1380
131 gtgaccgcgg gcgggtgtcag ggggaagcag atcacgctct ccctcggcga gcacgagagc      1440
132 aagggtctatg gcgccggcac ccgggtatcg gcatacagcc ccgaagcgcg caacaccacg      1500
133 aagatccgcg tgcactacaa cgtgggcctc gggcacagca tcgcgatccg cggcgacgag      1560
134 taccgcgttca cctggacctc cggccgaggc gcgcgcaacg tcgcgtccga cgtctgggag      1620
135 ttcgaggctc agcgcacccc cgacggtgag accttccagt tcaagcctct gatcgacgac      1680
136 gtcacctggt cgaccggcgg caacttcacc gggacgggcg gcgacgtgat cgacatctac      1740
137 cccaccttc      1749
139 <210> SEQ ID NO: 4
140 <211> LENGTH: 9
141 <212> TYPE: PRT
142 <213> ORGANISM: Arthrobacter globiformis
144 <400> SEQUENCE: 4
145 His Ile Gln Arg Leu Thr Ala Ile Lys
146   1           5
148 <210> SEQ ID NO: 5
149 <211> LENGTH: 13
150 <212> TYPE: PRT
151 <213> ORGANISM: Arthrobacter globiformis
153 <400> SEQUENCE: 5
154 Asp Met Glu Ser Phe Asp Gln Asn Ser Asn Leu Tyr Lys

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155      1              5              10
157 <210> SEQ ID NO: 6
158 <211> LENGTH: 10
159 <212> TYPE: PRT
160 <213> ORGANISM: Arthrobacter globiformis
162 <400> SEQUENCE: 6
163 Leu Gly Asp Leu Phe Asp Gln Asp Ser Lys
164      1              5              10
166 <210> SEQ ID NO: 7
167 <211> LENGTH: 27
168 <212> TYPE: PRT
169 <213> ORGANISM: Arthrobacter globiformis
171 <400> SEQUENCE: 7
172 Met Ile Leu Asp Val Val Pro Asn His Thr Ala Asp Tyr Leu Ala Gly
173      1              5              10              15
174 Thr Ser Thr Thr Tyr Ser Pro Ser Thr Tyr Lys
175              20              25
177 <210> SEQ ID NO: 8
178 <211> LENGTH: 20
179 <212> TYPE: PRT
180 <213> ORGANISM: Arthrobacter globiformis
182 <400> SEQUENCE: 8
183 Asp Trp Val Asp Met Gly Phe Asp Gly Ile Arg Val Asp Ala Ala Arg
184      1              5              10              15
185 Ser Val Pro Lys
186              20
188 <210> SEQ ID NO: 9
189 <211> LENGTH: 30
190 <212> TYPE: PRT
191 <213> ORGANISM: Arthrobacter globiformis
193 <400> SEQUENCE: 9
194 Tyr Ala Asn Pro Asn Arg Leu Glu Thr Phe Leu Asp Asn His Asp Arg
195      1              5              10              15
196 Ala Arg Phe Leu Thr Trp Ala Asp Asp Asn Tyr Gln Arg Leu
197              20              25              30
199 <210> SEQ ID NO: 10
200 <211> LENGTH: 4467
201 <212> TYPE: DNA
202 <213> ORGANISM: Arthrobacter globiformis
204 <400> SEQUENCE: 10
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206 ctggcgaccg cagccggcga ggcacctctc ctccgcccgg ccgacctcgt ctacctcggc      120
207 gtcgatctcg cgcagacgac ggaggagaaa cggtcgcagc gggaggcgct cgggctcgct      180
208 gtcgtcgagc agaacgctct cgtcgccgat cctcggcgag ctgctcggac cgcacgagcc      240
209 cacctcgccc caggaccgtt catcgtgcac ctggacgtcg atgtgctgga cttcctcgac      300
210 gcaccacctg ccgagaacgt gaacggccga aacagcgggc cgaccgtcga gcagctgcgg      360
211 gtcgcactcg ccagcttctt gcagcatccg gactgctggg cgatgtccat cggccagggtg      420
212 gtccccgcgc acgcggcggc cgaccgcacc tccatccgcg ggctcatcgg cgccctggcc      480
213 gtgagctcca cgtagccgga cgtcgctcct ggagcgggag cgctccggca ggaacggcgt      540

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214	cgcaccccgct	cgagcggggg	cgtcgccttc	ttcgacgggg	tctgcggcgc	ggctaccgcg	600
215	gcggcagcgt	gagccgccac	cgaccagatc	tcattgcattt	ggacgaactt	cgccgtccaa	660
216	ttctctccgc	gcctcaagca	ggtatacatc	gctcgaacgc	gtcttctactg	gcctgacggt	720
217	ccgcgatcac	gtcgtgcagt	gaagcatcct	gccgcgaagg	gtcttgatgc	gcatgcagta	780
218	cgggagtcga	atcactttca	cgggcacggc	cggtgtcagt	acttgacaaa	acgcatttat	840
219	acatgttgca	tcgatccagt	aaaccgtgca	gctcgcggac	cgatgcgcat	ccgacaacga	900
220	agtcaggaga	gagtc atg	aga acg	aca gtt	cgt acc	gct cgc	951
221		Met Arg	Thr Thr	Val Arg	Thr Ala	Arg Val	
222		1		5		10	
224	cgt acg	ggc ctc	gcg atg	gga gca	gcc gtc	gcg ctg	999
225	Arg Thr	Gly Leu	Ala Met	Gly Ala	Ala Val	Ala Leu	
226		15		20		25	
228	ctc acc	tgg ggc	acc ggc	ccc gca	ccc gcg	agt gcc	1047
229	Leu Thr	Trp Gly	Thr Gly	Pro Ala	Pro Ala	Ser Ala	
230		30		35		40	
232	tcg ccc	ggc ccg	ctg gcc	gag ggc	gac gtg	atc tac	1095
233	Ser Pro	Gly Pro	Leu Ala	Glu Gly	Asp Val	Ile Tyr	
234	45		50		55		
236	gac cgg	ttc gaa	gac ggc	gac ccc	acc aac	aac gac	1143
237	Asp Arg	Phe Glu	Asp Gly	Asp Pro	Thr Asn	Asn Asp	
238		65		70		75	
240	gag tac	gat ccg	tcc gac	ctc ggt	ttc tac	cac gcc	1191
241	Glu Tyr	Asp Pro	Ser Asp	Leu Gly	Phe Tyr	His Gly	
242		80		85		90	
244	ggc ctg	acg gac	cgg ctc	gac tac	atc gcc	gat ctg	1239
245	Gly Leu	Thr Asp	Arg Leu	Asp Tyr	Ile Ala	Asp Leu	
246		95		100		105	
248	atc tgg	ctc tcg	ccc gtc	tcc gag	cag cag	ccg ctc	1287
249	Ile Trp	Leu Ser	Pro Val	Ser Glu	Gln Gln	Pro Leu	
250		110		115		120	
252	ctg gag	gcc agc	tac cac	ggc tac	ttc act	cgg gac	1335
253	Leu Glu	Ala Ser	Tyr His	Gly Tyr	Phe Thr	Arg Asp	
254	125		130		135		
256	aac gag	cat ttc	ggc gac	cga gcc	gag ctg	cag gag	1383
257	Asn Glu	His Phe	Gly Asp	Arg Ala	Glu Leu	Gln Glu	
258		145		150		155	
260	gcg cac	gat ctc	gga ctc	aag atg	atc ctc	gac gtc	1431
261	Ala His	Asp Leu	Gly Leu	Lys Met	Ile Leu	Asp Val	
262		160		165		170	
264	acg gcc	gac tac	ctc gcg	ggc aca	tcg acg	acc tat	1479
265	Thr Ala	Asp Tyr	Leu Ala	Gly Thr	Ser Thr	Thr Tyr	
266		175		180		185	
268	tac aag	ccg gcg	agt ccg	ctc gat	gac gcg	tcg tac	1527
269	Tyr Lys	Pro Ala	Ser Pro	Leu Asp	Asp Ala	Ser Tyr	
270		190		195		200	
272	ggc gac	tgc ctg	ttc aac	ggg ctc	gag acg	cag acc	1575
273	Gly Asp	Cys Leu	Phe Asn	Gly Leu	Glu Thr	Gln Ile	
274	205		210		215		
276	tgc gac	ctc ggc	ggg ctc	gac gac	ctc gat	cag tcg	1623

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date